

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/771,395A

Source: IFW/b

Date Processed by STIC: 2/8/07

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 02/08/2007

PATENT APPLICATION: US/10/771,395A

TIME: 11:02:08

Input Set : A:\10-771,395 Sequence Listing.txt

Output Set: N:\CRF4\02082007\J771395A.raw

3 <110> APPLICANT: BERGERON, Dominique  
 4 DEHBI, Mohammed  
 5 DUBOW, Michael  
 6 GROS, Philippe  
 7 MCCARTY, John  
 8 PELLETIER, Jerry  
 10 <120> TITLE OF INVENTION: INHIBITORS OF STAPHYLOCOCCUS AUREUS PRIMARY SIGMA FACTOR AND  
 USES  
 11 THEREOF  
 13 <130> FILE REFERENCE: Q79408  
 15 <140> CURRENT APPLICATION NUMBER: 10/771,395A  
 16 <141> CURRENT FILING DATE: 2004-02-05  
 18 <150> PRIOR APPLICATION NUMBER: US 60/445,441  
 19 <151> PRIOR FILING DATE: 2003-02-07  
 21 <160> NUMBER OF SEQ ID NOS: 41  
 23 <170> SOFTWARE: PatentIn version 3.2  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1107  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Staphylococcus aureus  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(1107)  
 35 <400> SEQUENCE: 1  
 36 atg tct gat aac aca gtt aaa att aaa aaa caa aca att gat ccg aca 48  
 37 Met Ser Asp Asn Thr Val Lys Ile Lys Lys Gln Thr Ile Asp Pro Thr  
 38 1 5 10 15  
 40 tta àca tta gaa gat gtt aag aag caa tta att gaa aaa ggt aaa aaa 96  
 41 Leu Thr Leu Glu Asp Val Lys Lys Gln Leu Ile Glu Lys Gly Lys Lys  
 42 20 25 30  
 44 gag ggt cat tta agt cat gaa gaa att gct gaa aaa ctt cag aat ttt 144  
 45 Glu Gly His Leu Ser His Glu Glu Ile Ala Glu Lys Leu Gln Asn Phe  
 46 35 40 45  
 48 gat atc gac tct gat caa atg gat gat ttc ttt gat caa tta aat gat 192  
 49 Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp  
 50 50 55 60  
 52 aat gat att tca cta gtt aat gaa aaa gat agt tca gat act gac gag 240  
 53 Asn Asp Ile Ser Leu Val Asn Glu Lys Asp Ser Ser Asp Thr Asp Glu  
 54 65 70 75 80  
 56 aaa ctg aat cca agt gat ctt agt gcc cct cca ggt gtt aaa ata aat 288  
 57 Lys Leu Asn Pro Ser Asp Leu Ser Ala Pro Pro Gly Val Lys Ile Asn  
 58 85 90 95  
 60 gac cca gtt cgt atg tac ctt aaa gaa att ggg cgt gtt aac tta tta 336  
 61 Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val Asn Leu Leu

*see p. 6*

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62	100	105	110	
64	agt gca caa gaa gaa atc gaa tta gcc aaa cgt att gaa caa ggt gat	384		
65	Ser Ala Gln Glu Glu Ile Glu Leu Ala Lys Arg Ile Glu Gln Gly Asp			
66	115 120 125			
68	gaa gta gca aaa tca aga ctt gca gaa gcg aac tta cgt tta gtt gta	432		
69	Glu Val Ala Lys Ser Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val			
70	130 135 140			
72	agt att gct aaa aga tac gta ggt cgt ggt atg tta ttc ctt gat tta	480		
73	Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe Leu Asp Leu			
74	145 150 155 160			
76	atc caa gaa ggt aat atg ggt ctt att aaa gct gtt gaa aaa ttt gac	528		
77	Ile Gln Glu Gly Asn Met Gly Leu Ile Lys Ala Val Glu Lys Phe Asp			
78	165 170 175			
80	ttt aac aaa gga ttt aag ttt tca aca tat gca aca tgg tgg att aga	576		
81	Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg			
82	180 185 190			
84	caa gca atc act cgt gca att gct gac caa gca cgt acg att cgt atc	624		
85	Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile			
86	195 200 205			
88	cct gtg cat atg gta gaa aca att aat aaa tta att cgt gtt caa cgt	672		
89	Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val Gln Arg			
90	210 215 220			
92	caa tta tta cag gac tta ggt cga gat cca gca cca gaa gaa att ggt	720		
93	Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu Ile Gly			
94	225 230 235 240			
96	gaa gaa atg gat tta cca gca gaa aaa gtt cgt gaa att tta aaa att	768		
97	Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu Lys Ile			
98	245 250 255			
100	gcg caa gaa cct gtt tca tta gaa aca cca att ggt gaa gaa gat gat	816		
101	Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu Asp Asp			
102	260 265 270			
104	agt cat tta gga gac ttt att gag gat cag gaa gca caa agt cct tca	864		
105	Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser Pro Ser			
106	275 280 285			
108	gat cat gct gct tat gaa tta tta aaa gag caa tta gaa gat gtg ctt	912		
109	Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu Asp Val Leu			
110	290 295 300			
112	gat aca tta act gat aga gaa gaa aat gta tta cga tta aga ttt ggt	960		
113	Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu Arg Phe Gly			
114	305 310 315 320			
116	ctt gat gac ggc aga aca aga aca ctt gaa gaa gtt ggt aaa gtt ttc	1008		
117	Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe			
118	325 330 335			
120	ggt gtt aca cgt gaa cgt att cga caa att gaa gca aaa gca ctt aga	1056		
121	Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg			
122	340 345 350			
124	aaa tta aga cat cca agt cgt agt aaa cgt ttg aaa gac ttt atg gat	1104		
125	Lys Leu Arg His Pro Ser Arg Ser Lys Arg Leu Lys Asp Phe Met Asp			
126	355 360 365			

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Input Set : A:\10-771,395 Sequence Listing.txt

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```

128 taa
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 368
133 <212> TYPE: PRT
134 <213> ORGANISM: Staphylococcus aureus
136 <400> SEQUENCE: 2
138 Met Ser Asp Asn Thr Val Lys Ile Lys Lys Gln Thr Ile Asp Pro Thr
139 1 5 10 15
142 Leu Thr Leu Glu Asp Val Lys Lys Gln Leu Ile Glu Lys Gly Lys Lys
143 20 25 30
146 Glu Gly His Leu Ser His Glu Glu Ile Ala Glu Lys Leu Gln Asn Phe
147 35 40 45
150 Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp
151 50 55 60
154 Asn Asp Ile Ser Leu Val Asn Glu Lys Asp Ser Ser Asp Thr Asp Glu
155 65 70 75 80
158 Lys Leu Asn Pro Ser Asp Leu Ser Ala Pro Pro Gly Val Lys Ile Asn
159 85 90 95
162 Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val Asn Leu Leu
163 100 105 110
166 Ser Ala Gln Glu Glu Ile Glu Leu Ala Lys Arg Ile Glu Gln Gly Asp
167 115 120 125
170 Glu Val Ala Lys Ser Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
171 130 135 140
174 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe Leu Asp Leu
175 145 150 155 160
178 Ile Gln Glu Gly Asn Met Gly Leu Ile Lys Ala Val Glu Lys Phe Asp
179 165 170 175
182 Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg
183 180 185 190
186 Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile
187 195 200 205
190 Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val Gln Arg
191 210 215 220
194 Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu Ile Gly
195 225 230 235 240
198 Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu Lys Ile
199 245 250 255
202 Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu Asp Asp
203 260 265 270
206 Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser Pro Ser
207 275 280 285
210 Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu Asp Val Leu
211 290 295 300
214 Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu Arg Phe Gly
215 305 310 315 320
218 Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe
219 325 330 335
222 Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg

```

1107

## RAW SEQUENCE LISTING

DATE: 02/08/2007

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TIME: 11:02:08

Input Set : A:\10-771,395 Sequence Listing.txt

Output Set: N:\CRF4\02082007\J771395A.raw

```

223          340          345          350
226 Lys Leu Arg His Pro Ser Arg Ser Lys Arg Leu Lys Asp Phe Met Asp
227          355          360          365
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 242
232 <212> TYPE: PRT
233 <213> ORGANISM: Staphylococcus aureus
235 <400> SEQUENCE: 3
237 Gly Asp Glu Val Ala Lys Ser Arg Leu Ala Glu Ala Asn Leu Arg Leu
238 1          5          10          15
241 Val Val Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe Leu
242          20          25          30
245 Asp Leu Ile Gln Glu Gly Asn Met Gly Leu Ile Lys Ala Val Glu Lys
246          35          40          45
249 Phe Asp Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
250          50          55          60
253 Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile
254 65          70          75          80
257 Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val
258          85          90          95
261 Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu
262          100          105          110
265 Ile Gly Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu
266          115          120          125
269 Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu
270          130          135          140
273 Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser
274 145          150          155          160
277 Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu Asp
278          165          170          175
281 Val Leu Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu Arg
282          180          185          190
285 Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys
286          195          200          205
289 Val Phe Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala
290          210          215          220
293 Leu Arg Lys Leu Arg His Pro Ser Arg Ser Lys Arg Leu Lys Asp Phe
294 225          230          235          240
297 Met Asp
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 75
303 <212> TYPE: PRT
304 <213> ORGANISM: Staphylococcus aureus
306 <400> SEQUENCE: 4
308 Glu Leu Leu Lys Glu Gln Leu Glu Asp Val Leu Asp Thr Leu Thr Asp
309 1          5          10          15
312 Arg Glu Glu Asn Val Leu Arg Leu Arg Phe Gly Leu Asp Asp Gly Arg
313          20          25          30
316 Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe Gly Val Thr Arg Glu

```

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Input Set : A:\10-771,395 Sequence Listing.txt

Output Set: N:\CRF4\02082007\J771395A.raw

```

317          35          40          45
320 Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg Lys Leu Arg His Pro
321          50          55          60
324 Ser Arg Ser Lys Arg Leu Lys Asp Phe Met Asp
325 65          70          75
328 <210> SEQ ID NO: 5
329 <211> LENGTH: 67
330 <212> TYPE: PRT
331 <213> ORGANISM: Staphylococcus aureus
333 <400> SEQUENCE: 5
335 Glu Leu Leu Lys Glu Gln Leu Glu Asp Val Leu Asp Thr Leu Thr Asp
336 1          5          10          15
339 Arg Glu Glu Asn Val Leu Arg Leu Arg Phe Gly Leu Asp Asp Gly Arg
340          20          25          30
343 Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe Gly Val Thr Arg Glu
344          35          40          45
347 Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg Lys Leu Arg His Pro
348          50          55          60
351 Ser Arg Ser
352 65
355 <210> SEQ ID NO: 6
356 <211> LENGTH: 597
357 <212> TYPE: DNA
358 <213> ORGANISM: Bacteriophage G1
361 <220> FEATURE:
362 <221> NAME/KEY: CDS
363 <222> LOCATION: (1)..(597)
365 <400> SEQUENCE: 6
366 atg aaa tta aag att tta gat aaa gat aat gca aca ctt aat gtg ttt      48
367 Met Lys Leu Lys Ile Leu Asp Lys Asp Asn Ala Thr Leu Asn Val Phe
368 1          5          10          15
370 cat cgt aat aag gag cac aaa aca ata gat aat gta cca act gct aac      96
371 His Arg Asn Lys Glu His Lys Thr Ile Asp Asn Val Pro Thr Ala Asn
372          20          25          30
374 tta gtt gat tgg tac cct cta agt aat gct tat gag tac aag tta agt      144
375 Leu Val Asp Trp Tyr Pro Leu Ser Asn Ala Tyr Glu Tyr Lys Leu Ser
376          35          40          45
378 aga aac ggg gaa tac tta gaa tta aaa aga tta cgt tct act tta cct      192
379 Arg Asn Gly Glu Tyr Leu Glu Leu Lys Arg Leu Arg Ser Thr Leu Pro
380          50          55          60
382 tca tct tat ggt tta gat gat aat aac caa gat att att aga gat aat      240
383 Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn
384 65          70          75          80
386 aac cat aga tgt aaa ata ggt tat tgg tac aac cct gca gta cgc aaa      288
387 Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys
388          85          90          95
390 gat aat tta aag att ata gag aaa gct aaa caa tat gga tta cct att      336
391 Asp Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Ile
392          100          105          110

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/771,395A

DATE: 02/08/2007  
TIME: 11:02:09

Input Set : A:\10-771,395 Sequence Listing.txt  
Output Set: N:\CRF4\02082007\J771395A.raw

*FSI*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 6,12,16,17,19,25,27,31,32,34,35,36,40,41,46,48,49,50,51,53  
Seq#:11; N Pos. 54,55,56,57,60,62,66,68,69,70,71,72,73,75,81,82,83,84,85,86  
Seq#:11; N Pos. 91,94,95,99,105,109,111,112,113,117,124,125,126,134,135,137  
Seq#:11; N Pos. 139,140,144,145,146,147,148,151,153,158,166,169,177,178,180  
Seq#:11; N Pos. 181,186,187,188,198,199,201,204,205,206,207,208,209,210,211  
Seq#:11; N Pos. 212,213,214,219,220,221,223,224,225,227,234,235,236,243,245  
Seq#:11; N Pos. 248,249,250,251,252,256,257,258,263,265,271,272,273,274,276  
Seq#:11; N Pos. 277,278,286,288,294,295,297,307,308,315,322,327,334,336,340  
Seq#:11; N Pos. 341,342,343,344,346,348,349,350,354,357,358,360,363,367,368  
Seq#:11; N Pos. 370,372,373,375,376,377,378,384,387,388,389,390,391,392,393  
Seq#:11; N Pos. 394,396,400,403,405,406,409,413,415,417,420,421,426,428,433  
Seq#:11; N Pos. 434,435,437,438,439,440,441,442,443,444,445,447,448,449,450  
Seq#:11; N Pos. 452,453,459,461,462,463,465,466,467,468,469,470,474,475,477  
Seq#:11; N Pos. 481,482,483,484,487,488,492,493,495,496,501,502,503,508,509  
Seq#:11; N Pos. 510,511,512,514,516,517,520,521,522,525,529,530,534,535,540  
Seq#:11; N Pos. 546,552,558,562,570,574,576,582,585  
Seq#:12; Xaa Pos. 6,7,9,10,11,12,14,16,18,19,20,21,23,24,25,28,29,31,32,33  
Seq#:12; Xaa Pos. 37,42,45,46,47,48,49,50,51,53,60,63,67,68,69,70,71,72,73  
Seq#:12; Xaa Pos. 74,76,77,78,79,81,82,83,84,86,88,89,91,92,93,96,99,103  
Seq#:12; Xaa Pos. 108,112,114,115,116,117,119,120,123,124,125,126,130,131  
Seq#:12; Xaa Pos. 134,135,136,137,138,143,145,146,147,148,149,150,151,153  
Seq#:12; Xaa Pos. 154,155,156,157,159,161,162,163,165,166,167,168,170,171  
Seq#:12; Xaa Pos. 172,173,174,177,178,182,184,192

## VERIFICATION SUMMARY

DATE: 02/08/2007

PATENT APPLICATION: US/10/771,395A

TIME: 11:02:09

Input Set : A:\10-771,395 Sequence Listing.txt

Output Set: N:\CRF4\02082007\J771395A.raw

L:1248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:60  
L:1252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:120  
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:180  
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:240  
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:300  
L:1260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:360  
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:420  
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:480  
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:540  
L:1600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16  
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:32  
L:1612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48  
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:64  
L:1620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:80  
L:1624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:96  
L:1628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:112  
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:128  
L:1636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:144  
L:1640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:160  
L:1644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:176